

SEQUENCE LISTING

<110> Microscience Limited

<120> GENES AND PROTEINS, AND THEIR USE

<130> REP05973WO

<140>

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<160> 35

<170> PatentIn Ver. 2.1

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<211> 587

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1) .. (582)

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gat att tac tca cgt ctt tta aaa gat cgt att att atg ttg aca ggc	96
Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Ile Met Leu Thr Gly	
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caa gtt gag gat aat atg gcc aat agt atc att gca cag tta ttg ttt	144
Gln Val Glu Asp Asn Met Ala Asn Ser Ile Ile Ala Gln Leu Leu Phe	
35 40 45	

ctc gat gca caa gat aat aca aag gat att tac ctt tat gtc aat aca	192
Leu Asp Ala Gln Asp Asn Thr Lys Asp Ile Tyr Leu Tyr Val Asn Thr	
50 55 60	

cca ggt ggt tca gta tcg gct gga ctt gct att gtg gac acc atg aac	240
Pro Gly Gly Ser Val Ser Ala Gly Leu Ala Ile Val Asp Thr Met Asn	
65 70 75 80	

ttc att aaa tcg gac gta cag acg att gtt atg ggg atg gct gct tcg	288
Phe Ile Lys Ser Asp Val Gln Thr Ile Val Met Gly Met Ala Ala Ser	
85 90 95	

atg gga acc att att gct tca agt ggt gct aaa gga aaa cgt ttt atg 336
 Met Gly Thr Ile Ile Ala Ser Ser Gly Ala Lys Gly Lys Arg Phe Met
 100 105 110

tta ccg aat gca gaa tat atg atc cac caa cca atg ggc gga aca ggc 384
 Leu Pro Asn Ala Glu Tyr Met Ile His Gln Pro Met Gly Gly Thr Gly
 115 120 125

gga ggt aca cag caa tct gat atg gct atc gct gct gag cat ctt tta 432
 Gly Gly Thr Gln Gln Ser Asp Met Ala Ile Ala Ala Glu His Leu Leu
 130 135 140

aaa acg cgt cat act tta gaa aaa atc tta gct gat aat tct ggt caa 480
 Lys Thr Arg His Thr Leu Glu Lys Ile Leu Ala Asp Asn Ser Gly Gln
 145 150 155 160

tct att gaa aaa gtc cat gat gat gca gag cgt gat cgt tgg atg agt 528
 Ser Ile Glu Lys Val His Asp Asp Ala Glu Arg Asp Arg Trp Met Ser
 165 170 175

gct caa gaa aca ctt gat tat ggc ttt att gat gaa atc atg gct aat 576
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 180 185 190

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 Asn Glu

<210> 2

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<213> group B streptococcus

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 20 25 30

Gln Val Glu Asp Asn Met Ala Asn Ser Ile Ile Ala Gln Leu Leu Phe
 35 40 45

Leu Asp Ala Gln Asp Asn Thr Lys Asp Ile Tyr Leu Tyr Val Asn Thr
 50 55 60

Pro Gly Gly Ser Val Ser Ala Gly Leu Ala Ile Val Asp Thr Met Asn

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gct tgt gat ata ata gtc aat gtg agg agg act atc atg tta ttt aag      96
Ala Cys Asp Ile Ile Val Asn Val Arg Arg Thr Ile Met Leu Phe Lys
          20             25             30

gaa aaa att cct gga cta ata tta tgc ttt att att gct ata cca tct     144
Glu Lys Ile Pro Gly Leu Ile Leu Cys Phe Ile Ile Ala Ile Pro Ser

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35

40

45

tgg ttg ctt ggg ctt tat ctc cct tta ata gga gca cca gtc ttt gct 192
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<213> group B streptococcus

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Glu Lys Ile Pro Gly Leu Ile Leu Cys Phe Ile Ile Ala Ile Pro Ser
 35 40 45

Trp Leu Leu Gly Leu Tyr Leu Pro Leu Ile Gly Ala Pro Val Phe Ala
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Ile Leu Ile Gly Ile Ile Val Gly
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<222> (1)..(705)

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tta gct tat gga gct atc act tta gta gcc ctt ttt tca tgt att ttg 96
 Leu Ala Tyr Gly Ala Ile Thr Leu Val Ala Leu Phe Ser Cys Ile Leu
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gct gta acg gtc atc ttt aaa agt tca caa gtt act act gaa tct ttg 144
 Ala Val Thr Val Ile Phe Lys Ser Ser Gln Val Thr Thr Glu Ser Leu
 35 40 45

tca aaa gca gat aaa gtt cgc gta gcc aaa aaa tca aaa atg act aag 192
 Ser Lys Ala Asp Lys Val Arg Val Ala Lys Lys Ser Lys Met Thr Lys
 50 55 60

gcg aca tct aaa tca aaa gta gaa gat gta aaa cag gct cca aaa cct 240
 Ala Thr Ser Lys Ser Lys Val Glu Asp Val Lys Gln Ala Pro Lys Pro
 65 70 75 80

tct cag gca tct aat gaa gcc cca aaa tca agt tct caa tct aca gaa 288
 Ser Gln Ala Ser Asn Glu Ala Pro Lys Ser Ser Ser Gln Ser Thr Glu
 85 90 95

gct aat tct cag caa caa gtt act gcg agt gaa gag acg gct gta gaa 336
 Ala Asn Ser Gln Gln Gln Val Thr Ala Ser Glu Glu Thr Ala Val Glu
 100 105 110

caa gca gtt gta aca gaa ata ccc ctg cta cca gtc agg cac aac aac 384
 Gln Ala Val Val Thr Glu Ile Pro Leu Leu Pro Val Arg His Asn Asn
 115 120 125

ctt tat gct gtt act gag aca cct tac aac cct gct caa cca cca gac 432
 Leu Tyr Ala Val Thr Glu Thr Pro Tyr Asn Pro Ala Gln Pro Pro Asp
 130 135 140

caa gtg gcc agg tat gag caa tgg aaa tac tgc cag gcg gtc gga tct 480
 Gln Val Ala Arg Tyr Glu Gln Trp Lys Tyr Cys Gln Ala Val Gly Ser
 145 150 155 160

gct gct gca gca caa atg gct gct gca aca gga gtc cct cag tct act 528
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 165 170 175

tgg gaa cat att att gcc cgt gaa tca aat ggt aat cct aat gtt gct 576
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 180 185 190

aat gcc tca gga gct tca gga ctt ttc caa acg atg cca ggt tgg ggt 624
 Asn Ala Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly
 195 200 205

tca aca gct aca gtt cag gat caa gta att cag cta tta aag ctt att 672
 Ser Thr Ala Thr Val Gln Asp Gln Val Ile Gln Leu Leu Lys Leu Ile
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<212> PRT

<213> group B streptococcus

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Ala Val Thr Val Ile Phe Lys Ser Ser Gln Val Thr Thr Glu Ser Leu
 35 40 45

Ser Lys Ala Asp Lys Val Arg Val Ala Lys Lys Ser Lys Met Thr Lys
 50 55 60

Ala Thr Ser Lys Ser Lys Val Glu Asp Val Lys Gln Ala Pro Lys Pro
 65 70 75 80

Ser Gln Ala Ser Asn Glu Ala Pro Lys Ser Ser Ser Gln Ser Thr Glu
 85 90 95

Ala Asn Ser Gln Gln Gln Val Thr Ala Ser Glu Glu Thr Ala Val Glu
 100 105 110

Gln Ala Val Val Thr Glu Ile Pro Leu Leu Pro Val Arg His Asn Asn
 115 120 125

Leu Tyr Ala Val Thr Glu Thr Pro Tyr Asn Pro Ala Gln Pro Pro Asp
 130 135 140

Gln Val Ala Arg Tyr Glu Gln Trp Lys Tyr Cys Gln Ala Val Gly Ser
 145 150 155 160

Ala Ala Ala Ala Gln Met Ala Ala Ala Thr Gly Val Pro Gln Ser Thr
 165 170 175

Trp Glu His Ile Ile Ala Arg Glu Ser Asn Gly Asn Pro Asn Val Ala
 180 185 190

Asn Ala Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly
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gcc att cct gaa ttg ttg gaa ttc gat att acc gtt cgt gga gac aac 96
 Ala Ile Pro Glu Leu Leu Glu Phe Asp Ile Thr Val Arg Gly Asp Asn
 20 25 30

cgt gga tgg ttc aaa gag aac ttt caa aaa gaa aaa atg ata ccg ctt 144
 Arg Gly Trp Phe Lys Glu Asn Phe Gln Lys Glu Lys Met Ile Pro Leu
 35 40 45

ggt ttc cca gaa agc ttc ttt gag gca gac aaa cta caa aat aat att 192
 Gly Phe Pro Glu Ser Phe Phe Glu Ala Asp Lys Leu Gln Asn Asn Ile
 50 55 60

tcg ttt aca aaa aaa aat act ttg cga ggt ctc cat gca gag cct tgg 240
 Ser Phe Thr Lys Lys Asn Thr Leu Arg Gly Leu His Ala Glu Pro Trp
 65 70 75 80

gat aaa tat gtt tcg atc gct gat gaa gga cgt gtg atc ggt act tgg 288
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9

20 25 30
 gtt tat gga gat att ggt aca agc cca ctc tat acg atg caa tca ttg 144
 Val Tyr Gly Asp Ile Gly Thr Ser Pro Leu Tyr Thr Met Gln Ser Leu
 35 40 45
 gtt gaa aac caa ggt ggt att tct agt gtc aca gaa tcg ttt atc tta 192
 Val Glu Asn Gln Gly Gly Ile Ser Ser Val Thr Glu Ser Phe Ile Leu
 50 55 60
 ggt tct ata tct tta atc ata tgg acc ttg aca ctt att aca act atc 240
 Gly Ser Ile Ser Leu Ile Ile Trp Thr Leu Thr Leu Ile Thr Thr Ile
 65 70 75 80
 aag tat gtg ctt gta gct tta aag gcg gat aat cac cac gaa ggt ggt 288
 Lys Tyr Val Leu Val Ala Leu Lys Ala Asp Asn His His Glu Gly Gly
 85 90 95
 att ttt tct tta tat acc ctt gtt aga aaa atg aca cct tgg tta att 336
 Ile Phe Ser Leu Tyr Thr Leu Val Arg Lys Met Thr Pro Trp Leu Ile
 100 105 110
 gtt ccg gct gtt att gga ggt gca acc ttg ttg tca gat gga gct ttg 384
 Val Pro Ala Val Ile Gly Gly Ala Thr Leu Leu Ser Asp Gly Ala Leu
 115 120 125
 acg cca gct gta acc gta ctt cag ccg tta agg att aaa gta gtt cct 432
 Thr Pro Ala Val Thr Val Leu Gln Pro Leu Arg Ile Lys Val Val Pro
 130 135 140
 agt ttg cag cat att tcc aga atc aga gta tgt tat ttt gcg acc ttg 480
 Ser Leu Gln His Ile Ser Arg Ile Arg Val Cys Tyr Phe Ala Thr Leu
 145 150 155 160
 tta ttt act gtt act ttt gcc atc caa ggt ttg gaa cgg gtg tta ttg 528
 Leu Phe Thr Val Thr Phe Ala Ile Gln Gly Leu Glu Arg Val Leu Leu
 165 170 175
 gaa tta ttg gcc att atg tta tat ggt ttg cct ttt ggt tta 570
 Glu Leu Leu Ala Ile Met Leu Tyr Gly Leu Pro Phe Gly Leu
 180 185 190
 ncggtctcct tatagttttg cccatccaga agttttcaag cattaatcca tactacggtt 630
 tgaaattggt atttagtcca gagaatcata aaggatatattt tatttttag gat cta ttt 687
 Asp Leu Phe
 tcc tgg cga caa acg gga gca gaa gca cta tac tct gac tta ggt cat 735

Ser Trp Arg Gln Thr Gly Ala Glu Ala Leu Tyr Ser Asp Leu Gly His
 195 200 205

gtt ggg cgt gga aat ata cat gtt tca tgg ccg ttc gtt aag gtt gcc 783
 Val Gly Arg Gly Asn Ile His Val Ser Trp Pro Phe Val Lys Val Ala
 210 215 220 225

att ata ctt tct tat tgt ggg caa ggg gca tgg att tta gct aat aag 831
 Ile Ile Leu Ser Tyr Cys Gly Gln Gly Ala Trp Ile Leu Ala Asn Lys
 230 235 240

aac gca gga aat gaa ttg aat ccc ttt ttt gct agt att cct tcg caa 879
 Asn Ala Gly Asn Glu Leu Asn Pro Phe Phe Ala Ser Ile Pro Ser Gln
 245 250 255

ttt aca atg cat gtc gtt att tta gct act ttg gca gct atc atc gct 927
 Phe Thr Met His Val Val Ile Leu Ala Thr Leu Ala Ala Ile Ile Ala
 260 265 270

tca cag gca ctg att tct ggatcaattt accttaagtt ctgagctatg 975
 Ser Gln Ala Leu Ile Ser
 275

cgactaaaaa tattcccaca atttcgttca acttatcctg ttgacaatat tgggtcaaac 1035

ctacatacct ggtattaatt ggttcttatt tgccattaca acctctattg gtttgctttt 1095

taagacttca gcgcacatgg aagcagcata tggattagcg ataacaatta cgatgcta 1155

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<211> 190

<212> PRT

<213> group B streptococcus

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Ser Phe Asp Lys Ala Ser Lys Ala Gly Phe Ile Ile Ala Leu Gly Ile
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Val Tyr Gly Asp Ile Gly Thr Ser Pro Leu Tyr Thr Met Gln Ser Leu
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65

70

75

80

Ile Ile Ala Ser Gln Ala Leu Ile Ser

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<212> DNA

<213> group B streptococcus

<220>

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<222> (1)..(378)

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1				5					10					15		

cat	atg	ggt	tcg	gga	gtt	gtg	atg	cta	att	gtc	atg	aca	ggt	tta	gcc	96
His	Met	Gly	Ser	Gly	Val	Val	Met	Leu	Ile	Val	Met	Thr	Gly	Leu	Ala	
			20					25					30			

atg	ata	ttt	gga	gtg	aag	ttt	tct	aaa	gca	ctt	gaa	ggt	ggt	att	aag	144
Met	Ile	Phe	Gly	Val	Lys	Phe	Ser	Lys	Ala	Leu	Glu	Gly	Gly	Ile	Lys	
		35				40					45					

tta	gct	att	gct	ctt	acg	ggt	att	ggt	gct	att	att	ggt	att	tta	act	192
Leu	Ala	Ile	Ala	Leu	Thr	Gly	Ile	Gly	Ala	Ile	Ile	Gly	Ile	Leu	Thr	
	50					55					60					

ggt	gct	ttt	tcc	gaa	tca	ctt	caa	gct	ttt	gtt	aaa	aat	aca	gga	atc	240
Gly	Ala	Phe	Ser	Glu	Ser	Leu	Gln	Ala	Phe	Val	Lys	Asn	Thr	Gly	Ile	
65					70				75					80		

aat	cta	agc	att	att	gac	gtt	ggt	tgg	gct	cca	tta	gca	act	att	aca	288
Asn	Leu	Ser	Ile	Ile	Asp	Val	Gly	Trp	Ala	Pro	Leu	Ala	Thr	Ile	Thr	
			85					90					95			

tgg	gga	tca	cca	tat	acg	ctt	tac	ttc	tta	tta	atc	atg	ctt	att	gtc	336
Trp	Gly	Ser	Pro	Tyr	Thr	Leu	Tyr	Phe	Leu	Leu	Ile	Met	Leu	Ile	Val	
			100					105					110			

aat	att	gtt	atg	att	gtt	atg	aaa	aaa	aaa	cgg	ata	cct	tag			378
Asn	Ile	Val	Met	Ile	Val	Met	Lys	Lys	Lys	Arg	Ile	Pro				
		115				120					125					

<210> 13
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 <212> PRT
 <213> group B streptococcus

<400> 13
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 20 25 30
 Met Ile Phe Gly Val Lys Phe Ser Lys Ala Leu Glu Gly Gly Ile Lys
 35 40 45
 Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu Thr
 50 55 60
 Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly Ile
 65 70 75 80
 Asn Leu Ser Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile Thr
 85 90 95
 Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Ile Met Leu Ile Val
 100 105 110
 Asn Ile Val Met Ile Val Met Lys Lys Lys Arg Ile Pro
 115 120 125

<210> 14
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 <222> (118)..(705)

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 acatattgcc aaagttttga tattattact ataatatagt ttgtagagga gaataat 117

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	38.5	12.5	25	65	0.1	3.2	0.95
Gender	1.2	0.4	1	2	0.0	3.0	0.98
Marital Status	1.5	0.5	1	3	0.2	3.1	0.96
Education	12.5	2.5	9	16	0.3	3.3	0.94
Income	1500	500	1000	2500	0.4	3.4	0.93
Occupation	1.8	0.6	1	3	0.1	3.2	0.95
Health Status	1.2	0.4	1	2	0.0	3.0	0.98
Stress Level	2.5	1.0	1	4	0.5	3.5	0.92
Life Satisfaction	3.5	1.5	1	5	0.2	3.1	0.96
Resilience	2.8	1.2	1	4	0.3	3.3	0.94
Emotional Stability	3.2	1.0	1	4	0.1	3.2	0.95
Social Support	2.0	0.8	1	3	0.2	3.1	0.96
Work-Life Balance	2.5	1.0	1	4	0.3	3.3	0.94
Overall Well-being	3.0	1.2	1	4	0.2	3.1	0.96

cta tca tct tag
 Leu Ser Ser
 195

705

<210> 15
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 <213> group B streptococcus

<400> 15

Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr
 1 5 10 15

Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly
 20 25 30

Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
 35 40 45

Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
 50 55 60

Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
 65 70 75 80

Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr
 85 90 95

Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu
 100 105 110

Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu
 115 120 125

Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln
 130 135 140

Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile
 145 150 155 160

Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu
 165 170 175

Gly Ile Gln Asp Phe Ser Gln Val Ser Ser Gly Arg Asn Gly Gly Lys
 180 185 190

Leu Ser Ser

195

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 Thr Ile Ala Leu Ser Tyr Leu Leu Gly Ser Ser Ile Trp Leu Phe Ile
 20 25 30
 gta cag ttt att gct tac tat gta tct gga att tat ttt tat aaa tta 144
 Val Gln Phe Ile Ala Tyr Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu
 35 40 45
 gtt tat tat gtg gca caa agt gaa att gtc tcg ata ggc atg acg ttg 192
 Val Tyr Tyr Val Ala Gln Ser Glu Ile Val Ser Ile Gly Met Thr Leu
 50 55 60
 att ttc tat ata atg aat att gtc tta gga ttc ggt ggt atg tac cca 240
 Ile Phe Tyr Ile Met Asn Ile Val Leu Gly Phe Gly Gly Met Tyr Pro
 65 70 75 80
 ata cag tgg gca tta cct ttt atg ctc att tcg cta tgg ttt tta att 288
 Ile Gln Trp Ala Leu Pro Phe Met Leu Ile Ser Leu Trp Phe Leu Ile
 85 90 95
 aaa ttt tgt gtc gat aat atc gtt gat gaa gca ttt ata ttt tat ggt 336
 Lys Phe Cys Val Asp Asn Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly
 100 105 110
 att tta gca gca ttc tca cta ttt ata gat c 367
 Ile Leu Ala Ala Phe Ser Leu Phe Ile Asp
 115 120

<210> 17

Ile Pro Tyr Ser Asp Val Phe Ala Thr Gly Gly Phe Leu Tyr Tyr Val
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Val Gln Phe Ile Ala Tyr Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu .
35 40 45

Ile Phe Tyr Ile Met Asn Ile Val Leu Gly Phe Gly Gly Met Tyr Pro
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Lys Phe Cys Val Asp Asn Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly
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<210> 18
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1 5 10 15

18

gat gct aat tct agg cag agt gtt acc tac acc aaa gaa gaa ttt ata 144
 Asp Ala Asn Ser Arg Gln Ser Val Thr Tyr Thr Lys Glu Glu Phe Ile
 35 40 45

caa aaa att gtg cca gat gcg caa gat cta gga aag tcg tac ggt att 192
 Gln Lys Ile Val Pro Asp Ala Gln Asp Leu Gly Lys Ser Tyr Gly Ile
 50 55 60

cgt cct tca ttt att att gca cag gcg gct ttg gat tct gat ttc gga 240
 Arg Pro Ser Phe Ile Ile Ala Gln Ala Ala Leu Asp Ser Asp Phe Gly
 65 70 75 80

gag aaa tat agc tat agt atc ata atc tgt tgg ttg ctt gca gaa cca 288
 Glu Lys Tyr Ser Tyr Ser Ile Ile Ile Cys Trp Leu Leu Ala Glu Pro
 85 90 95

gga acg ccc tca att acc tta aat gat agt agt aca gga aaa aaa cag 336
 Gly Thr Pro Ser Ile Thr Leu Asn Asp Ser Ser Thr Gly Lys Lys Gln
 100 105 110

gaa aag caa ttt act cat tat aaa tct tgg aag tat tca atg gat gat 384
 Glu Lys Gln Phe Thr His Tyr Lys Ser Trp Lys Tyr Ser Met Asp Asp
 115 120 125

tac ctt gct cat ata aaa tct gga gcg aca ggc aaa aaa gat tca tat 432
 Tyr Leu Ala His Ile Lys Ser Gly Ala Thr Gly Lys Lys Asp Ser Tyr
 130 135 140

act ata atg gtg tct gtt aaa aat cca aaa act tta gtg caa aaa tta 480
 Thr Ile Met Val Ser Val Lys Asn Pro Lys Thr Leu Val Gln Lys Leu
 145 150 155 160

caa gat agt ggt ttt gat aat gac aaa aag tac gct aaa aaa atg acg 528
 Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
 165 170 175

gaa atc att gat ttg tat gat tta aca aga tat gat aag tga 570
 Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
 180 185 190

<210> 19

<211> 189

<212> PRT

<213> group B streptococcus

<400> 19

Met Arg Lys Arg Phe Ser Leu Leu Asn Phe Ile Val Val Thr Phe Ile
 1 5 10 15

Phe Phe Phe Phe Ile Leu Phe Pro Leu Leu Asn His Lys Gly Lys Val
 20 25 30

Asp Ala Asn Ser Arg Gln Ser Val Thr Tyr Thr Lys Glu Glu Phe Ile
 35 40 45

Gln Lys Ile Val Pro Asp Ala Gln Asp Leu Gly Lys Ser Tyr Gly Ile
 50 55 60

Arg Pro Ser Phe Ile Ile Ala Gln Ala Ala Leu Asp Ser Asp Phe Gly
 65 70 75 80

Glu Lys Tyr Ser Tyr Ser Ile Ile Ile Cys Trp Leu Leu Ala Glu Pro
 85 90 95

Gly Thr Pro Ser Ile Thr Leu Asn Asp Ser Ser Thr Gly Lys Lys Gln
 100 105 110

Glu Lys Gln Phe Thr His Tyr Lys Ser Trp Lys Tyr Ser Met Asp Asp
 115 120 125

Tyr Leu Ala His Ile Lys Ser Gly Ala Thr Gly Lys Lys Asp Ser Tyr
 130 135 140

Thr Ile Met Val Ser Val Lys Asn Pro Lys Thr Leu Val Gln Lys Leu
 145 150 155 160

Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
 165 170 175

Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
 180 185

<210> 20

<211> 978

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(978)

<400> 20

atg ctt gtc atc att ttg atc att gta cta gct agt ctg aca gtg acg 48
 Met Leu Val Ile Ile Leu Ile Ile Val Leu Ala Ser Leu Thr Val Thr
 1 5 10 15

ata att tct tac cca aaa atg acg gaa tta aca aag tcc gtt gaa aaa 96
 Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys
 20 25 30

caa ctt gaa gat aat gct gat aat cta tca gac caa ctg aca tat cag 144
 Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln
 35 40 45

ata gaa gtg gcg caa aaa gat caa atc tac gtg act aat cag cta aac 192
 Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn
 50 55 60

cgt atg caa cag gaa att atc agt cgc tta ccg ata tgc gta cag aat 240
 Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn
 65 70 75 80

aaa tca gca tta acg gag agt cga gat cga tca gac aaa cgc ttg gaa 288
 Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu
 85 90 95

ttg att aac tcc aat tta tct cag tca gtt cag aaa atg caa gat tca 336
 Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser
 100 105 110

atg aaa aac gct tgg atc aaa tgc gcc aaa ctg ttg agg aaa agc tgg 384
 Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp
 115 120 125

aaa aaa cgc tac aaa cgc gtt gca aac ttc ttt gaa act gta tcg cgt 432
 Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg
 130 135 140

caa cta gag agc gtc aat caa ggt ctg ggt aga tgg aaa ctg tgc caa 480
 Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln
 145 150 155 160

gat gtt ggt acc act gaa caa agt ctg tca aat act aag aca agg gga 528
 Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly
 165 170 175

ata tta ggg gag tta caa ctc ggt caa att ata gaa gat att atg aca 576
 Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr
 180 185 190

gtt agt caa tat gag aga gaa ttt cct acg gtg tct ggc tct tct gag 624
 Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu
 195 200 205

cgt gtt gaa tat gct att aaa tac ctg gaa atg gtc agg gag att ata 672
 Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile
 210 215 220

tct att tgc cta ttg act cta agt ttc tct aga aga tta tta ccg att 720
 Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile
 225 230 235 240

ggg aga tgc tta tgg aat tgg gtg acc agg ttc aaa tgg aac tct att 768
 Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile
 245 250 255

cgt aat ctt tac tgg gca agt att cgt aaa ttt gca aaa gat ata aac 816
 Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn
 260 265 270

aat aag tac tta aat cct cct gaa acg aca aat ttt ggt atc atg ttc 864
 Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

tta cca act gaa ggg ctc tat tct gaa gtg gta aga aat gca aca ttc 912
 Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
 290 295 300

ttt gat agt cta aga cgt gac gaa aat att gta gta gct gga ccg tca 960
 Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
 305 310 315 320

acc tta tct gct tac taa 978
 Thr Leu Ser Ala Tyr
 325

<210> 21

<211> 325

<212> PRT

<213> group B streptococcus

<400> 21

Met Leu Val Ile Ile Leu Ile Ile Val Leu Ala Ser Leu Thr Val Thr
 1 5 10 15

Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys
 20 25 30

Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln
 35 40 45
 Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn
 50 55 60
 Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn
 65 70 75 80
 Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu
 85 90 95
 Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser
 100 105 110
 Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp
 115 120 125
 Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg
 130 135 140
 Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln
 145 150 155 160
 Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly
 165 170 175
 Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr
 180 185 190
 Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu
 195 200 205
 Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile
 210 215 220
 Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile
 225 230 235 240
 Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile
 245 250 255
 Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn
 260 265 270
 Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
 290 295 300

Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
 305 310 315 320

Thr Leu Ser Ala Tyr
 325

<210> 22

<211> 579

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(579)

<400> 22

atg cga aaa gaa gtg aca cca gag atg ctt aac tat aat aag tat cct 48
 Met Arg Lys Glu Val Thr Pro Glu Met Leu Asn Tyr Asn Lys Tyr Pro
 1 5 10 15

ggc cca cag ttt att cac ttt gaa aat atc gtt aaa agt gat gat att 96
 Gly Pro Gln Phe Ile His Phe Glu Asn Ile Val Lys Ser Asp Asp Ile
 20 25 30

gaa ttt caa ctt gtt att aat gaa aaa tca gct ttt gat gtg act gtc 144
 Glu Phe Gln Leu Val Ile Asn Glu Lys Ser Ala Phe Asp Val Thr Val
 35 40 45

ttt gga caa cgt ttt tct gag att tta tta aaa tat gat ttt atc gtt 192
 Phe Gly Gln Arg Phe Ser Glu Ile Leu Leu Lys Tyr Asp Phe Ile Val
 50 55 60

ggc gat tgg ggt aac gag cag ttg agg cta aga ggc ttt tac aaa gat 240
 Gly Asp Trp Gly Asn Glu Gln Leu Arg Leu Arg Gly Phe Tyr Lys Asp
 65 70 75 80

gct agt acg att aga aaa aat agc cgg att tca cgt tta gaa gat tat 288
 Ala Ser Thr Ile Arg Lys Asn Ser Arg Ile Ser Arg Leu Glu Asp Tyr
 85 90 95

att aaa gag tat tgt aac ttt ggt tgt gct tat ttt gtg ttg gag aat 336
 Ile Lys Glu Tyr Cys Asn Phe Gly Cys Ala Tyr Phe Val Leu Glu Asn

aaa gct gtt ttt aaa ggt tca gat aac tat aaa gtc act ttt aaa aaa 240
 Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys
 65 70 75 80

aca gaa tgg tca tcg gta ttt acc ggc att gat tca gga aag ttt caa 288
 Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln
 85 90 95

atg ggt gga aat aat att tct tat tca tca gag aga tct caa aaa tay 336
 Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr
 100 105 110

tta ttt tca tac cca ata ggc tct act cct tca gtt tta gca gtt cct 384
 Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro
 115 120 125

aag aat agt aat atc aaa gct tat aat gat att agt ggt cat aaa aca 432
 Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr
 130 135 140

cag gtt gtc caa gga acg aca act gcc aag caa tta gaa aat ttc aat 480
 Gln Val Val Gln Gly Thr Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn
 145 150 155 160

aaa gag cat cag aaa aat cct gtt act cta aaa tat act aat gaa aat 528
 Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
 165 170 175

att aca cag att cta acg aat ttg agt gat gga aaa gct gat ttt aaa 576
 Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
 180 185 190

ctt ttg acg gac caa ctg tta acg cta tta taa 609
 Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
 195 200

<210> 25

<211> 202

<212> PRT

<213> group B streptococcus

<400> 25

Met Thr Ile Lys Lys Val Leu Ser Val Thr Gly Ile Ile Leu Val Thr
 1 5 10 15

Val Ala Ser Leu Ala Ala Cys Ser Ser Lys Ser His Thr Thr Lys Thr
 20 25 30

Gly Lys Lys Glu Val Asn Phe Ala Thr Val Gly Thr Thr Ala Pro Phe
 35 40 45

Ser Tyr Val Lys Asp Gly Lys Leu Thr Gly Phe Asp Ile Glu Val Ala
 50 55 60

Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys
 65 70 75 80

Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln
 85 90 95

Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr
 100 105 110

Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro
 115 120 125

Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr
 130 135 140

Gln Val Val Gln Gly Thr Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn
 145 150 155 160

Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
 165 170 175

Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
 180 185 190

Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
 195 200

<210> 26

<211> 357

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(357)

<400> 26

atg aag aat ata aca aag cta tca act gtt gct tta agc cta cta ctt 48
 Met Lys Asn Ile Thr Lys Leu Ser Thr Val Ala Leu Ser Leu Leu Leu

[illegible]

<211> 118

<212> PRT

<213> group B streptococcus

<400> 27

Met Lys Asn Ile Thr Lys Leu Ser Thr Val Ala Leu Ser Leu Leu Leu
1 5 10 15

Cys Thr Ala Cys Ala Ala Ser Asn Thr Ser Thr Ser Lys Thr Gln Ser
20 25 30

His His Pro Lys Gln Thr Lys Leu Thr Asp Lys Gln Lys Glu Glu Pro
35 40 45

Lys Asn Lys Glu Ala Ala Asp Gln Glu Met His Pro Gln Gly Ala Val
50 55 60

Asp Leu Thr Lys Tyr Lys Ala Lys Pro Val Lys Asp Tyr Gly Lys Lys
65 70 75 80

Ile Asp Val Gly Asp Gly Lys Lys Met Asn Ile Tyr Glu Thr Gly Gln
85 90 95

Gly Lys Ile Pro Ile Val Phe Ile Pro Gly Gln Ala Glu Ile Arg His
100 105 110

Ala Met Leu Ile Arg Ile
115

<210> 28

<211> 1191

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1)..(1191)

<400> 28

gtg aat gaa tcg acc atc aga aaa gaa ttt aaa ata gtt gtt ttt aaa 48
Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
1 5 10 15

tgg atc tta aat aat caa gca gtt att gct ctc atg att acc ttt ttg 96
Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
20 25 30

gta ttt tta acg att ttt att ttt acc aaa atc tct ttt atg ttt aaa 144
Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys
35 40 45

cct gtg ttt gat ttt ctt gct gtg ctg ata ttg ccg ctt gta att tct 192
Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser
50 55 60

ggc ttg ctt tat tac cta tta aaa cct atg gtt aca ttt tta gag aag 240
Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys
65 70 75 80

cgg gga att aag cgt gta aca gcg ata tta tca gtt ttt act att ata 288
Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile
85 90 95

atc ctt ctg tta att tgg gca atg tct agt ttt att ccc atg atg agt 336
 Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser
 100 105 110

aat caa tta cgc cat ttt atg gaa gat ctc cct tca tat gtg aat aaa 384
 Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys
 115 120 125

gtg caa atg gaa aca agt tcg ttt ata gat cac aac cct tgg tta aaa 432
 Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys
 130 135 140

tct tat aaa ggg gaa ata tcg agc atg tta tct aat atc agt agc caa 480
 Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln
 145 150 155 160

gcg gtc tct tat gct gaa aaa ttt tca aag aat gtt tta gat tgg gca 528
 Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala
 165 170 175

gga aat tta gct agt aca gtt gca cgt gtg aca gta gca aca atc atg 576
 Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met
 180 185 190

gct ccc ttt att ttg ttt tat ctt tta aga gat agt cgc aac atg aag 624
 Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys
 195 200 205

aat ggt ttc tta atg gtt tta cca acc aaa cta cgc caa cca gct gat 672
 Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp
 210 215 220

cgt att ttg cga gaa atg aat agt caa atg tca gga tat gtg caa gga 720
 Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly
 225 230 235 240

caa atc att gtt gct att act gtt ggt gtt att ttt tca ata atg tat 768
 Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr
 245 250 255

agt att ata ggc ctt aga tat ggc gtg aca tta ggg att att gcc ggt 816
 Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly
 260 265 270

gtg tta aat atg gtt ccc tat ttg gga agt ttt gtc gcc caa att cca 864
 Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro
 275 280 285

gtg ttt atc tta gcg ctt gtc gca gga cct gtt atg gtt gtt aaa gtt 912
 Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val
 290 295 300

gcg att gtt ttt gtt att gag caa act cta gag gga cgc ttt gtc tca 960
 Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser
 305 310 315 320

cct ttg gtt tta ggt aat aaa ctt agc att cat cca att aca att atg 1008
 Pro Leu Val Leu Gly Asn Lys Leu Ser Ile His Pro Ile Thr Ile Met
 325 330 335

ttt att tta tta acc tct gga gcg atg ttt ggt gtt tgg gga gta ttc 1056
 Phe Ile Leu Leu Thr Ser Gly Ala Met Phe Gly Val Trp Gly Val Phe
 340 345 350

ctc agt att ccg att tat gca tct atc aaa gtt gtt gtt aaa gaa ttg 1104
 Leu Ser Ile Pro Ile Tyr Ala Ser Ile Lys Val Val Val Lys Glu Leu
 355 360 365

ttt gat tgg tac aaa gct gtc agt ggg cta tat aca ata gat gtt gtt 1152
 Phe Asp Trp Tyr Lys Ala Val Ser Gly Leu Tyr Thr Ile Asp Val Val
 370 375 380

act gaa gaa aga agt gaa gaa gtt aaa aat gtt gaa tag 1191
 Thr Glu Glu Arg Ser Glu Glu Val Lys Asn Val Glu
 385 390 395

<210> 29

<211> 396

<212> PRT

<213> group B streptococcus

<400> 29

Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
 1 5 10 15

Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
 20 25 30

Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys
 35 40 45

Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser
 50 55 60

Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys
65 70 75 80

Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile
85 90 95

Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser
100 105 110

Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys
115 120 125

Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys
130 135 140

Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln
145 150 155 160

Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala
165 170 175

Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met
180 185 190

Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys
195 200 205

Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp
210 215 220

Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly
225 230 235 240

Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr
245 250 255

Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly
260 265 270

Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro
275 280 285

Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val
290 295 300

Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser
305 310 315 320

35

Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg
 275 280 285
 gac ttt gtt ttc atg agg ctt gtt aag ctt tta gtt aaa aat aaa gtt 912
 Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val
 290 295 300
 ttt aaa aac cgt aat gtt act tca agt gta gct tat att atc aat atg 960
 Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
 305 310 315 320
 ctt ctt atg gga ttc tgg cat ggg tta act tgg tac tat ata gcc tat 1008
 Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
 325 330 335
 ggt ctc ttt cat ggg att ggc cta gtt att aat gac gct tgg gta cgt 1056
 Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
 340 345 350
 aag aag aaa aat ayt aat aaa gaa aga aga ttg gct aaa aaa cca ctt 1104
 Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
 355 360 365
 tta cca gaa aac aaa tgg act tat gct ttg ggt gtc ttc atc acc ttt 1152
 Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
 370 375 380
 aat gta gtt atg ttt tct ttc ttg att ttt tca gga ttt tta gat ctt 1200
 Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
 385 390 395 400
 ttg tgg ttc cca caa ccg cat aac aaa taa 1230
 Leu Trp Phe Pro Gln Pro His Asn Lys
 405 410

<210> 31

<211> 409

<212> PRT

<213> group B streptococcus

<400> 31

Met Phe Met Gly Ile Pro Gln Tyr Phe Phe Tyr Leu Ile Leu Ala Val
 1 5 10 15

Leu Pro Ile Tyr Ile Gly Leu Phe Phe Lys Lys Arg Phe Ala Leu Tyr
 20 25 30

Glu Ile Ile Phe Ser Leu Ser Phe Ile Val Met Met Leu Thr Gly Ser
 35 40 45
 Thr Phe Asn Gln Leu Lys Ser Leu Leu Ala Tyr Val Val Gly Gln Ser
 50 55 60
 Leu Leu Val Phe Ile Tyr Lys Ala Tyr Arg Lys Arg Phe Asn His Thr
 65 70 75 80
 Leu Val Phe Tyr Val Thr Val Cys Leu Ser Ile Phe Pro Leu Phe Leu
 85 90 95
 Val Lys Leu Ile Pro Ala Ile Ser Glu Asp Gly His Gln Ser Leu Phe
 100 105 110
 Gly Phe Leu Gly Ile Ser Tyr Leu Thr Phe Arg Ala Val Ala Met Ile
 115 120 125
 Ile Glu Met Arg Asp Gly Val Leu Lys Glu Phe Thr Leu Trp Glu Phe
 130 135 140
 Leu Arg Phe Leu Leu Phe Phe Pro Thr Phe Ser Ser Gly Pro Ile Asp
 145 150 155 160
 Arg Phe Lys Arg Phe Asn Glu Asp Tyr Ile Asn Ile Pro Asp Arg Asn
 165 170 175
 Glu Leu Leu Asp Met Leu Gly Gln Ala Ile His Tyr Leu Met Leu Gly
 180 185 190
 Phe Leu Tyr Lys Phe Ile Leu Ala Tyr Ile Phe Gly Ser Leu Ile Met
 195 200 205
 Pro Pro Leu Lys Glu Leu Ala Leu Glu Gln Gly Gly Val Phe Asn Trp
 210 215 220
 Pro Thr Leu Gly Val Met Tyr Ala Phe Gly Phe Asp Leu Phe Phe Asp
 225 230 235 240
 Phe Ala Gly Tyr Thr Met Phe Ala Leu Ala Ile Ser Asn Leu Met Gly
 245 250 255
 Ile Lys Ser Pro Ile Asn Phe Asp Lys Pro Phe Lys Ser Arg Asp Leu
 260 265 270
 Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg
 275 280 285

Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val
 290 295 300

Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
 305 310 315 320

Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
 325 330 335

Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
 340 345 350

Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
 355 360 365

Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
 370 375 380

Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
 385 390 395 400

Leu Trp Phe Pro Gln Pro His Asn Lys
 405

<210> 32

<211> 100

<212> DNA

<213> group B streptococcus

<220>

<221> CDS

<222> (1) .. (99)

<400> 32

atg aat aaa ata acg aca tta tca acc atc gcc ctg act tta atg ctt 48
 Met Asn Lys Ile Thr Thr Leu Ser Thr Ile Ala Leu Thr Leu Met Leu
 1 5 10 15

tgc gtt gga tgt tct gcc aat aaa gat aat caa aaa act aaa act gag 96
 Cys Val Gly Cys Ser Ala Asn Lys Asp Asn Gln Lys Thr Lys Thr Glu
 20 25 30

gat c 100
 Asp

<210> 33
 <211> 33
 <212> PRT
 <213> group B streptococcus

<400> 33
 Met Asn Lys Ile Thr Thr Leu Ser Thr Ile Ala Leu Thr Leu Met Leu
 1 5 10 15

Cys Val Gly Cys Ser Ala Asn Lys Asp Asn Gln Lys Thr Lys Thr Glu
 20 25 30

Asp

<210> 34
 <211> 654
 <212> DNA
 <213> group B streptococcus

<220>
 <221> CDS
 <222> (1) .. (654)

<400> 34
 gat cga ggc tat caa gaa gca atg gct aaa cta agg aaa act tac ggc 48
 Asp Arg Gly Tyr Gln Glu Ala Met Ala Lys Leu Arg Lys Thr Tyr Gly
 1 5 10 15

gaa tat ggt tta ggg gtt tct aca gga tta gat tta cct gaa tca gaa 96
 Glu Tyr Gly Leu Gly Val Ser Thr Gly Leu Asp Leu Pro Glu Ser Glu
 20 25 30

ggt tat gta cct gga aaa tac agc tta gga aca act cta atg gaa tcg 144
 Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu Met Glu Ser
 35 40 45

ttc ggt cag tat gat gcc tat aca cca atg caa ctt ggt cag tat atc 192
 Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly Gln Tyr Ile
 50 55 60

tca act att gcg aat aat ggg aat cgt tta gca cct cac gtg gtt tca 240
 Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His Val Val Ser
 65 70 75 80

gat atc tat gaa ggg aat gat tct aat aag ttc gct caa ttg gtt cgt 288

Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln Leu Val Arg
 85 90 95

tca atc act cct aaa aca cta aat aag ata gct atc tca gat caa gag 336
 Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
 100 105 110

tta gcc att att caa gaa ggt ttt tat aac gtt gtc aat agt gga agt 384
 Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
 115 120 125

ggc tat gca act ggt acg tca atg agg ggg aat gtg aca acc att agy 432
 Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Xaa
 130 135 140

ggt aaa act ggt acc gct gaa aca ttt gct aaa aat ata aat gga caa 480
 Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
 145 150 155 160

aca gtt tct acc tac aac tta aac gct att gcc tac gat act aat cgt 528
 Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
 165 170 175

aaa ata gca gta gcg gta atg tat ccg cat gtt aca act gat aca aca 576
 Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
 180 185 190

aaa tcc cat caa tta gtt gca cga gat atg att gat caa tat att tca 624
 Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
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 Gln Ser Gln Asp Asn Lys Arg Gly His
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Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu Met Glu Ser
 35 40 45
 Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly Gln Tyr Ile
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 Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His Val Val Ser
 65 70 75 80
 Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln Leu Val Arg
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 Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
 100 105 110
 Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
 115 120 125
 Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Xaa
 130 135 140
 Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
 145 150 155 160
 Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
 165 170 175
 Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
 180 185 190
 Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
 195 200 205
 Gln Ser Gln Asp Asn Lys Arg Gly His
 210 215